

ALIGNMENTS									
4	4983	99.0	5414	6	CS043118	Sequence			
5	4983	99.0	5414	8	AB00656	AB00656 Homo sapi			
6	4980	98.9	3302	6	CO84222	Sequence			
7	4971.5	98.8	5371	8	HS250014	AJ750014 Homo sapi			
8	4968.5	98.7	3311	6	CQB4226	CQB4226 Sequence			
9	4962	98.6	3480	6	CQ719792	Sequence			
10	4942	98.2	4527	6	BD221207	BD221207 Human cyt			
11	4718.5	93.7	4314	9	AK122389	AK122389 Mus muscu			
12	4718.5	93.7	4501	9	BC042438	BC042438 Mus muscu			
13	4712	93.6	3267	9	BC082001	BC082001 Rattus no			
14	4601	91.4	2845	6	BD160617	BD160617 Primer fo			
15	4601	91.4	2845	6	AX883937	AX883937 Sequence			
16	4601	91.4	2845	8	AK024348	AK024348 Homo sapi			
c	18	4600.5	91.4	241990	14	AC123449	AC123449 Rattus no		
c	18	4600.5	91.4	251132	14	AC098162	AC098162 Rattus no		
RESULT 1									
LOCUS	CQ834224	3302 bp	DNA						
DEFINITION	Sequence 95 from Patent	WO2004058805.							
ACCESSION	Sequence 95								
VERSION	CQ834224								
KEYWORDS	CQ834224.1	GI:50833761							
SOURCE	Homo sapiens (human)								
ORGANISM	Homo sapiens								
MATERIAL	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.								
REFERENCE	1								
AUTHORS	Matsuda, A. and Yoneta, S.								
TITLE	T cell activating gene								
JOURNAL	Patent: WO 2004058805-A 95 15-JUL-2004;								
FEATURES	Asahi Kasei Pharma Corporation (JP)								
source	Location/Qualifiers								
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	/note="unnamed protein product"								
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	/protein_id="CAH053327.1"								
	/db_xref="GI:50833762"								
	/translation="MSGGLSQBERTSPYBPERIFYLQLQBCSVTDKOTQKLKVKPGSIGQTQDRSYGHSHRSPAKKRNQGLKILEQPHAVLFDYBQDKVYNEKFTELIAITNCBFRSLFKRNQRLSLSKGLQIDVQCPVQVRSCEBKFQCVVRGPPLAERTVSGIFGVVLEEBRGQGFTGQVQDFGVFLDKLELIEDDTALDESITAGPGDTMVOELPLEINRSVLSRKGTEGETSGTVI.FCDVLPKGKESLGYFVGVDMDNPIGNWDGRFDVQVLCSFACVESTLILHINDLIPESVTOERPPKLAFLMSRGVGDKGSSSHNKPATGTSFSDPGRNRSSELFYTNGSSYDQPSLTKMPTNTGSPSLQSAQSMBELNTAPDRSSPLQPPVNSLTTENRPHSLPSLTKMPTNTGSPSLQSAQSMBELNTAPVOESPPLAMPQGNQSGLEVSLSLAEVKENPFPYGVLRWIGQPGLNEVNLAGILEDECA GCTDGTPRGRYFTCALKALFQKPSLQSPASLQPSVNOERCNSLAFGGYLSE VVEVYSETOBLLRVEINPRLRIVYCATKIMKURKILKEVAAAGFTSPSEKDPPEF KATGTSFSDPGRNRSSELFYTNGSSYDQPSLTKMPTNTGSPSLQSAQSMBELNTAPUNLFHHLRVEPLLIKSAQKDFKLFKIFPSLIELNTDTPROCRIGGLAMYECCR KPAEAFPSCLLQMPRFQGDPLKDFKLFKIFPSLIELNTDTPROCRIGGLAMYECCR CYDDPDISACKIKOFEKTCNTQVHLHPKRLNHKYKNPVSLPKDLPDMDRHSCLPCOMMELFAVLCIETSYVAVKYGKDDSAWLFDSMADRGQNGENIPQVTCPCEVGTLKMSLEDQHSLSDRRIQCARLILCDAVMYQSPTMVLYK"								
Database :	GenBank	149.4	*						
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6:	gb_dat:	*							
7:	gb_ph:	*							
8:	gb_dr:	*							
9:	gb_ro:	*							
10:	gb_sts:	*							
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SUMMARIES									
Result No.	Score	Query Match	Length	DB ID	Description				
1	4983	99.0	3302	6	CQ834224	CQ834224 Sequence			
2	4983	99.0	3540	8	BC012342	BC012342 Homo sapi			
3	4983	99.0	5414	6	CS034166	CS034166 Sequence			
ORIGIN									
Alignment Scores:									
Pred. No.:	0								
Score:									
Percent Similarity:	4983.00								
Best Local Similarity:	99.48%								
Query Match:	98.99%								
DB:	6								
Length:	3302								
Matches:	948								
Mismatches:	0								
Indels:	1								
Gaps:	4								

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.